

**WHAT IS CLAIMED IS:**

1. An isolated polynucleotide comprising the nucleotide sequence that encodes a protein having the following amino acid sequence:

5 Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-  
Leu-Ser-Val-Ile-Met-Glu-Glu-Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-  
Gln-Leu-Ile-Lys-Asn-Phe-Thr-Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-  
Gly-Pro-Arg-Gly-Asp-Arg-Gly-Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-  
Asn-Lys-Gly-Gln-Lys-Gly-Glu-Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-  
10 Ala-Gly-Glu-Arg-Gly-Pro-Ile-Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-  
Gly-Gly-Lys-Gly-Ser-Lys-Gly-Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-  
Ser-Pro-Gly-Lys-Pro-Gly-Pro-Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-  
Pro-Gly-Pro-Pro-Gly-Lys-Glu-Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-  
Gly-Phe-Gln-Gly-Leu-Gln-Gly-Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-  
15 Pro-Arg-Gly-Leu-Pro-Gly-Leu-Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-  
Lys-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-  
Ala-Leu-Gln-Asn-Glu-Pro-Thr-Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-  
Pro-His-Trp-Lys-Asn-Phe-Thr-Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-  
Lys-Glu-Ile-Phe-Glu-Asp-Ala-Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-  
20 His-Leu-Val-Phe-Ile-Asn-Thr-Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-  
Gln-Met-Val-Gly-Arg-Glu-Ser-His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-  
Arg-Glu-Asn-Glu-Trp-Lys-Trp-Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-  
Asn-Trp-Lys-Ala-Gly-Gln-Pro-Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-  
Gly-Glu-Asp-Cys-Ala-Gly-Leu-Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-  
25 Gln-Cys-Glu-Asp-Val-Asn-Asn-Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-  
Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO:2, 206-547).

2. An isolated polynucleotide comprising the nucleotide sequence that

encodes a protein having the following amino acid sequence:

Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-Gln-Leu-Ile-Lys-Asn-Phe-Thr-  
Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-Gly-Pro-Arg-Gly-Asp-Arg-Gly-  
Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-Asn-Lys-Gly-Gln-Lys-Gly-Glu-  
5 Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-Ala-Gly-Glu-Arg-Gly-Pro-Ile-  
Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-Gly-Gly-Lys-Gly-Ser-Lys-Gly-  
Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-Ser-Pro-Gly-Lys-Pro-Gly-Pro-  
Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Lys-Glu-  
Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-Gly-Phe-Gln-Gly-Leu-Gln-Gly-  
10 Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-Pro-Arg-Gly-Leu-Pro-Gly-Leu-  
Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-Lys-Gly-Pro-Pro-Gly-Pro-Pro-  
Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-Ala-Leu-Gln-Asn-Glu-Pro-Thr-  
Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-Pro-His-Trp-Lys-Asn-Phe-Thr-  
Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-Lys-Glu-Ile-Phe-Glu-Asp-Ala-  
15 Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-His-Leu-Val-Phe-Ile-Asn-Thr-  
Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-Gln-Met-Val-Gly-Arg-Glu-Ser-  
His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-Arg-Glu-Asn-Glu-Trp-Lys-Trp-  
Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-Asn-Trp-Lys-Ala-Gly-Gln-Pro-  
Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-Gly-Glu-Asp-Cys-Ala-Gly-Leu-  
20 Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-Gln-Cys-Glu-Asp-Val-Asn-Asn-  
Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-Val-Leu-Ser-Ser-Ala-Leu (SEQ ID N  
O: 2, 229-547).

3. The polynucleotide according to claim 2, wherein said protein furt  
25 her comprises the following amino acid sequence upstream of the first methioni  
ne residue (SEQ ID NO:2, 229):

Met-Glu-Glu (SEQ ID NO: 2, 226-228); or

Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 211-228).

5           4. The polynucleotide according to claim 2, wherein said protein further comprises the following amino acid sequence upstream of the first methionine residue (SEQ ID NO:2, 229):

10 ~~Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-~~  
~~Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-~~  
~~Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-~~  
~~Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-~~  
~~Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-~~  
~~Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-~~  
~~Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-~~  
~~Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID N~~  
~~O: 102-228);~~

15 ~~Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-~~  
~~Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-~~  
~~His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-~~  
~~Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-~~  
~~Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-~~  
~~Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-~~  
~~Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-~~  
~~Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-~~  
~~Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 91-228);~~  
~~Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-~~

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Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-  
Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-  
Ile-Met-Glu-Glu (SEQ ID NO: 2, 1-228).

- 5            5.    An isolated polynucleotide comprising a nucleotide sequence having  
the following nucleotide sequence:

atgcaacaag atttgatgag gtcgagggtta gacactgaag tagccaactt atcagtgatt  
atggaagaaa tgaagctagt agaactccaag catggtcagc tcatacaagaa ttttacaata  
ctacaaggtc caccggggccc caggggtcca agaggtgaca gaggatccca gggaccccct  
ggcccaactg gcaacaaggg acagaaagga gagaaggggg agcctggacc acctggccct  
gcgggtgaga gaggcccaat tggaccagct ggtccccccg gagagcgtgg cggcaaagga  
tctaaaggct cccagggccc caaaggctcc cgtggttccc ctgggaagcc cggccctcag  
ggccccagtg gggacccagg cccccgggc ccaccaggca aagagggact ccccggccct  
cagggcctc ctggcttcca gggacttcag ggcaccgttg gggagcctgg ggtgcctgga  
cctcggggac tgccaggctt gcttggggta ccaggcatgc caggcccca gggccccccc  
ggcctcctg gccatcagg agcgggtgtg cccctggccc tgcagaatga gccaaacccg  
gcaccggagg acaatggctg cccgcctcac tggaagaact tcacagacaa atgtactat  
tttcagttg agaaagaaat ttttgaggat gcaaagcttt tctgtgaaga caagtcttca  
catcttgttt tcataaacac tagagaggaa cagcaatgga taaaaaaca gatggtaggg  
agagagagcc actggatcgg cctcacagac tcagagcgtg aaaatgaatg gaagtggctg  
gatgggacat ctccagacta caaaaattgg aaagctggac agccggataa ctggggtcac  
ggccatgggc caggagaaga ctgtgctggg ttgatttatg ctgggcagtg gaacgatttc  
caatgtgaag acgtcaataa cttcatttgc gaaaaagaca gggagacagt actgtcatct  
gcatta (SEQ ID NO: 1, 670-1695).

- 25            6.    An isolated polynucleotide comprising a nucleotide sequence having

the following nucleotide sequence:

atgaagctag tagactccaa gcatggtcag ctcataaga attttacaat actacaaggt  
 ccaccgggcc ccaggggtcc aagaggtgac agaggatccc agggaccccc tggcccaact  
 ggcaacaagg gacagaaagg agagaagggg gagcctggac cacctggccc tgcgggtgag  
 5 agaggcccaa ttggaccagc tgggtccccc ggagagcgtg gcggcaaagg atctaaaggc  
 tcccagggcc ccaaggctc cegtggttcc cctgggaagc ccggccctca gggccccagt  
 ggggaccag gcccccggg cccaccaggc aaagaggagc tcccggccc tcagggcct  
 cctggcttcc agggacttca gggcacggtt ggggagcctg ggggtgcctgg acctcgggga  
 ctgccaggct tgcttgggt accaggcatg ccaggcccca agggcccccc cgccctcct  
 10 ggcccatcag gagcgggtgt gccctggcc ctgcagaatg agccaacccc ggcaccggag  
 gacaatggct gccgcctca ctggaagaac ttacagaca aatgctacta tttttcagtt  
 gagaaagaaa tttttgagga tgcaagctt ttctgtgaag acaagtcttc acatcttgtt  
 ttcataaaca ctagagagga acagcaatgg ataaaaaac agatggtagg gagagagagc  
 cactggatcg gcctcacaga ctgagcgt gaaaatgaat ggaagtggct ggatgggaca  
 15 tctccagact acaaaaattg gaaagctgga cagcggata actggggtca tggccatggg  
 ccaggagaag actgtgctgg gttgatttat gctgggcagt ggaacgattt ccaatgtgaa  
 gacgtcaata acttcatttg cgaaaagac agggagacag tactgtcatc tgcatta  
 (SEQ ID NO: 1, 739-1695).

20 7. The polynucleotide according to claim 6 further comprises the following nucleotide sequence 5' upstream of said nucleotide sequence:

atggaagaa (SEQ ID NO: 1, 730-738); or

atgaggtcga ggtagacac tgaagtagcc aacttatcag tgattatgga agaa (SEQ ID NO: 1, 685-738).

25 8. The polynucleotide according to claim 6 further comprises the following

nucleotide sequence 5' upstream of said nucleotide sequence:

atggagaaca tcaccactat ctctcaagcc aacgagcaga acctgaaaga cctgcaggac  
ttacacaaag atgcagagaa tagaacagcc atcaagttca accaactgga ggaacgcttc  
cagctctttg agacggatat tgtgaacatc attagcaata tcagttacac agcccaccac  
5 ctgcggacgc tgaccagcaa tctaaatgaa gtcaggacca cttgcacaga tacccttacc  
aaacacacag atgatctgac ctcttgaat aataccctgg ccaacatccg tttggattct  
gtttctctca ggatgcaaca agatttgatg aggtcgaggt tagacactga agtagccaac  
ttatcagtga ttatggaaga a (SEQ ID NO: 1, 358-738);

atgaacagcc agctcaactc attcacaggt cagatggaga acatcaccac tatctctcaa  
10 gccaacgagc agaacctgaa agacctgcag gacttacaca aagatgcaga gaatagaaca  
gccatcaagt tcaaccaact ggaggaacgc ttccagctct ttgagacgga tattgtgaac  
atcattagca atatcagtta cacagccac cacctgcgga cgctgaccag caatctaaat  
gaagtcagga ccacttgcaac agataccctt accaaacaca cagatgatct gacctccttg  
aataataccc tggccaacat cggttggat tctgtttctc tcaggatgca acaagatttg  
15 atgaggtcga ggtagacac tgaagtagcc aacttatcag tgattatgga agaa (SEQ ID NO:  
1, 325-738);

atgaacctca acaacctgaa cctgaocag gtgcagcaga ggaacctcat cacgaatctg  
cagcggctctg tggatgacac aagcaggct atccagcga tcaagaacga ctttcaaact  
ctgcagcagg tttttcttca agccaagaag gacacggatt ggctgaagga gaaagtgcag  
20 agcttgcaga cgctggctgc caacaactct gcgttgcca aagccaacaa cgacaccctg  
gaggatatga acagccagct caactcattc acaggtcaga tggagaacat caccactatc  
tctcaagcca acgagcagaa cctgaaagac ctgcaggact tacacaaaga tgcagagaat  
agaacagcca tcaagttcaa ccaactggag gaacgcttcc agctctttga gacggatatt  
gtgaacatca ttagcaatat cagttacaca gccaccacc tgcggacgct gaccagcaat  
25 ctaaataag ttaggaccac ttgcacagat acccttacca aacacacaga tgatctgacc  
tccttgaata ataccctggc caacatccgt ttggattctg tttctctcag gatgcaacaa

gatttgatga ggtcgaggtt agacactgaa gtagccaact tatcagtgat tatggaagaa (SEQ I  
D NO: 1, 79-738);

atgtattctc ataatgtggt catcatgaac ctcaacaacc tgaacctgac ccaggtgcag  
cagaggaacc tcatcacgaa tctgcagcgg tctgtggatg acacaagcca ggctatccag  
5 cgaatcaaga acgactttca aaatctgcag caggtttttc ttcaagccaa gaaggacacg  
gattggctga aggagaaagt gcagagcttg cagacgctgg ctgccaacaa ctctgcgttg  
gccaaagcca acaacgacac cctggaggat atgaacagcc agctcaactc attcacaggt  
cagatggaga acatcaccac tatctctcaa gccaacgagc agaacctgaa agacctgcag

gacttacaca aagatgcaga gaatagaaca gccatcaagt tcaaccaact ggaggaacgc  
100 ttccagctct ttgagacgga tattgtgaac atcattagca atatcagtta cacagcccac  
cacctgcgga cgctgaccag caatctaaat gaagtcagga ccaattgac agataccctt  
accaaacaca cagatgatct gacotccttg aataataccc tggccaacat ccgtttggat  
tctgtttctc tcaggatgca acaagatttg atgaggtcga ggtagacac tgaagtagcc  
aacttatcag tgattatgga agaa (SEQ ID NO:1, 55-738); or

150 gtcacgaatc tgcagcaaga taccagcgtg ctccagggca atctgcagaa ccaaattgat  
tctcataatg tggatcatcat gaacctcaac aacctgaacc tgacctcaggt gcagcagagg  
aacctcatca cgaatctgca gcggctctgt gatgacacaa gccaggctat ccagcgaatc  
aagaacgact ttcaaaatct gcagcaggtt ttctttcaag ccaagaagga cacggattgg  
ctgaaggaga aagtgcagag cttgcagacg ctggctgcca acaactctgc gttggccaaa

20 gccaacaacg acacctgga ggatatgaac agccagctca actcattcac aggtcagatg  
gagaacatca ccaatatctc tcaagccaac gagcagaacc tgaaagacct gcaggactta  
caciaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttcag  
ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg  
cggacgctga ccagcaatct aatgaagtc aggaccactt gcacagatac ccttaccaaa  
25 cacacagatg atctgacctc cttgaataat acctggcca acatccgttt ggattctgtt  
tctctcagga tgcaacaaga ttgatgagg tcgaggttag aactgaagt agccaactta



tcagtgatta tggaagaa (SEQ ID NO: 1, 1-738).

9. The polynucleotide according to any one of claims 5 to 8 further comprises the following nucleotide sequence 3' downstream of said nucleotide sequence:

taacggactg tgatgggatac acatgagcaa attttcagct ctcaaaggca aaggacactc  
ctttctaatt gcatacactt ctcatcagat tgaaaaaaaaaaaagcactg aaaaccaatt  
actgaaaaaaaaaattgacagc tagtggtttttt taccatccgt cattacccaa agacttggga  
actaaaatgt tccccagggt gatatgctga ttttcattgt gcacatggac tgaatcacat  
agattctcct ccgtcagtaa ccgtgcgatt atacaaatta tgtcttccaa agtatggaac  
actccaatca gaaaaagggt atcatcccg (SEQ ID NO: 1, 1696-2024).

10. An isolated polynucleotide encoding a novel collectin, which can hybridize under a stringent condition with a probe that is an amplification product from PCR reaction performed using primers having the following nucleotide sequences:

caatctgatgagaaggatg (SEQ ID NO: 4) and  
acgaggggctggatgggacat (SEQ ID NO: 5).

11. A polynucleotide which can hybridize under a stringent condition with any one of the polynucleotide according to any one of claims 1 to 10, wherein the protein encoded by said polynucleotide is a novel collectin which comprises: (1)  $\text{Ca}^{2+}$ -dependent carbohydrate recognition domain (CRD), and (2) collagen-like region.

12. The polynucleotide according to any one of claims 1 to 11, wherein said polynucleotide is cDNA.

13. A novel collectin comprising the amino acid sequence encoded by the polynucleotide according to any one of claims 5 to 12.

14. A novel collectin comprising the amino acid sequence:

Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-  
Leu-Ser-Val-Ile-Met-Glu-Glu-Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-  
Gln-Leu-Ile-Lys-Asn-Phe-Thr-Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-  
Gly-Pro-Arg-Gly-Asp-Arg-Gly-Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-  
5 Asn-Lys-Gly-Gln-Lys-Gly-Glu-Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-  
Ala-Gly-Glu-Arg-Gly-Pro-Ile-Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-  
Gly-Gly-Lys-Gly-Ser-Lys-Gly-Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-  
Ser-Pro-Gly-Lys-Pro-Gly-Pro-Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-  
Pro-Gly-Pro-Pro-Gly-Lys-Glu-Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-  
10 Gly-Phe-Gln-Gly-Leu-Gln-Gly-Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-  
Pro-Arg-Gly-Leu-Pro-Gly-Leu-Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-  
Lys-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-  
Ala-Leu-Gln-Asn-Glu-Pro-Thr-Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-  
Pro-His-Trp-Lys-Asn-Phe-Thr-Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-  
15 Lys-Glu-Ile-Phe-Glu-Asp-Ala-Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-  
His-Leu-Val-Phe-Ile-Asn-Thr-Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-  
Gln-Met-Val-Gly-Arg-Glu-Ser-His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-  
Arg-Glu-Asn-Glu-Trp-Lys-Trp-Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-  
Asn-Trp-Lys-Ala-Gly-Gln-Pro-Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-  
20 Gly-Glu-Asp-Cys-Ala-Gly-Leu-Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-  
Gln-Cys-Glu-Asp-Val-Asn-Asn-Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-  
Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO: 2, 206-547).

15. A novel collectin comprising the amino acid sequence:

Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-Gln-Leu-Ile-Lys-Asn-Phe-Thr-  
Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-Gly-Pro-Arg-Gly-Asp-Arg-Gly-

Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-Asn-Lys-Gly-Gln-Lys-Gly-Glu-  
 Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-Ala-Gly-Glu-Arg-Gly-Pro-Ile-  
 Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-Gly-Gly-Lys-Gly-Ser-Lys-Gly-  
 Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-Ser-Pro-Gly-Lys-Pro-Gly-Pro-  
 5 Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Lys-Glu-  
 Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-Gly-Phe-Gln-Gly-Leu-Gln-Gly-  
 Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-Pro-Arg-Gly-Leu-Pro-Gly-Leu-  
 Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-Lys-Gly-Pro-Pro-Gly-Pro-Pro-  
 Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-Ala-Leu-Gln-Asn-Glu-Pro-Thr-  
 10 Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-Pro-His-Trp-Lys-Asn-Phe-Thr-  
 Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-Lys-Glu-Ile-Phe-Glu-Asp-Ala-  
 Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-His-Leu-Val-Phe-Ile-Asn-Thr-  
 Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-Gln-Met-Val-Gly-Arg-Glu-Ser-  
 His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-Arg-Glu-Asn-Glu-Trp-Lys-Trp-  
 15 Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-Asn-Trp-Lys-Ala-Gly-Gln-Pro-  
 Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-Gly-Glu-Asp-Cys-Ala-Gly-Leu-  
 Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-Gln-Cys-Glu-Asp-Val-Asn-Asn-  
 Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO: 2,  
 229-547).

16. The novel collectin according to claim 15, wherein said novel collectin  
 further comprises the following amino acid sequence upstream of the first methionine  
 residue (SEQ ID NO: 2, 229):

Met-Glu-Glu (SEQ ID NO: 2, 226-228); or

25 Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SE  
 Q ID NO: 2, 211-228).

17. The novel collectin according to claim 15, wherein said novel collectin further comprises the following amino acid sequence upstream of the first methionine residue (SEQ ID NO: 2, 229):

Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-  
5 Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-  
Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-  
Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-  
Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-  
Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-  
10 Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-  
Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2,  
102-228);

Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-  
Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-  
15 His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-  
Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-  
Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-  
Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-  
Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-  
20 Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-  
Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 91-228);

Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-  
Ile-Thr-Asn-Leu-Gln-Arg-Ser-Val-Asp-Asp-Thr-Ser-Gln-Ala-Ile-Gln-  
Arg-Ile-Lys-Asn-Asp-Phe-Gln-Asn-Leu-Gln-Gln-Val-Phe-Leu-Gln-Ala-  
25 Lys-Lys-Asp-Thr-Asp-Trp-Leu-Lys-Glu-Lys-Val-Gln-Ser-Leu-Gln-Thr-  
Leu-Ala-Ala-Asn-Asn-Ser-Ala-Leu-Ala-Lys-Ala-Asn-Asn-Asp-Thr-Leu-  
Glu-Asp-Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-

Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-  
Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-  
Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-  
Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-  
5 Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-  
Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-  
Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-  
Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 9-228); or  
Met-Tyr-Ser-His-Asn-Val-Val-Ile-Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-  
10 Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-Ile-Thr-Asn-Leu-Gln-Arg-Ser-Val-  
Asp-Asp-Thr-Ser-Gln-Ala-Ile-Gln-Arg-Ile-Lys-Asn-Asp-Phe-Gln-Asn-  
Leu-Gln-Gln-Val-Phe-Leu-Gln-Ala-Lys-Lys-Asp-Thr-Asp-Trp-Leu-Lys-  
Glu-Lys-Val-Gln-Ser-Leu-Gln-Thr-Leu-Ala-Ala-Asn-Asn-Ser-Ala-Leu-  
Ala-Lys-Ala-Asn-Asn-Asp-Thr-Leu-Glu-Asp-Met-Asn-Ser-Gln-Leu-Asn-  
15 Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-  
Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-  
Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-  
Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-  
His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-  
20 Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-  
Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-  
Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-  
Ile-Met-Glu-Glu (SEQ ID NO: 2, 1-228).

25 18. The novel collectin according to any one of claims 13 to 17, which is derived from human.

19. The novel collectin consisting of the amino acid sequence that comprises deletion, substitution and/or addition of one or more amino acids in the collectin according to any one of claims 13 to 18, and said novel collectin comprises (1)  $\text{Ca}^{2+}$ -dependent carbohydrate recognition domain (CRD), and (2) collagen-like region.

20. A vector which comprises the polynucleotide according to any one of the claims 1 to 12 in a manner that allows expression of the novel collectin.

21. A host cell comprising the vector according to claim 20 in a manner that allows the expression.

22. A probe for screening the novel collectin related molecular species comprising the polynucleotide according to any one of claims 1 to 12 or a fragment thereof.

23. An antibody having specific immunoreactivity with the novel collectin according to any one of claims 13 to 19.

24. The antibody according to claim 23, which is a monoclonal antibody.

25. The antibody according to claim 23 or 24 having reduced immunogenicity to human.

26. A method for obtaining a novel collectin related molecular species, comprising screening a protein using the antibody according to any one of claims 23 to 25.

27. A method for obtaining a novel collectin and/or derived molecules, comprising screening a protein using the antibody according to any one of claims 23 to 25.

28. The method according to claim 26 or 27, wherein said screening is expression screening of cDNA library.

29. A method of quantitative determination of a novel collectin and/or derived molecules, comprising measuring an amount of the novel collectin and/or derived molecules contained in a test sample using the antibody according to any one of claims 23 to 25.

30. The method according to claim 29, wherein said antibody is employed in ELISA method.

31. A kit for quantitative determination of a novel collectin and/or derived molecules, comprising the antibody according to any one of claims 23 to 25, wherein an amount of the novel collectin and/or derived molecules in a test sample is measured by ELISA method using the antibody.

32. A method for obtaining a novel collectin and/or derived molecules, comprising isolating a novel collectin and/or derived molecules using the antibody according to any one of claims 23 to 25.

33. The method according to claim 32, wherein affinity chromatography by a support bound with said antibody, and/or immunoprecipitation is utilized.

34. The method according to claim 32 or 33, comprising expressing the novel collectin from the polynucleotide according to any one of claims 1 to 12 prior to the isolation step.

35. A transgenic non-human animal that is stably introduced with a recombinant gene comprising the polynucleotide according to any one of claims 1 to 12 into the chromosome, and that can express a novel collectin.

36. A transgenic non-human animal wherein introduction of a gene is effected in a non-human animal comprising a homologue of the novel collectin according to any one of claims 13 to 19, in a manner to modify the gene expression of said homologue.

37. A knockout non-human animal that is obtained by altering a gene encoding a homologue of the novel collectin according to any one of claims 13 to 19 in a non-human animal comprising said homologue, in a manner to inhibit the expression of said homologue.

5

Add  
B<sup>2</sup>

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